

[illegible]

— 4 —

My residence, post office address and citizenship are as stated below next to my name;

"ISOLATED MAMMALIAN DENDRITIC CELL GENES: RELATED REAGENTS"
the specification of which

☒ was filed on November 26, 1997 as Application Serial No. 08/978,289

I acknowledge the duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, §1.56(a).

| | | | |
|-------------------------------|------------------|-------------------------------|------------------|
| Prior Foreign Application(s): | | | Priority Claimed |
| <u>(Number)</u> | <u>(Country)</u> | <u>(Day/Month/Year Filed)</u> | <u>Yes or No</u> |

| | |
|----------------------|--------------------------|
| <u>60/031,806</u> | <u>November 27, 1996</u> |
| (Application Number) | (Filing Date) |

| | |
|----------------------|--------------------------|
| <u>60/032,767</u> | <u>December 11, 1996</u> |
| (Application Number) | (Filing Date) |

I hereby claim the benefit under Title 35, United States Code, §120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, §1.56(a) which occurred between the filing date of the prior application and the national or PCT international filing date of this application:

| (Application Serial No.) | (Filing Date) | (Status – patented, pending, abandoned) |
|--------------------------|---------------|---|
| | | |

Power of Attorney: As a named inventor, I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and transact all business in Patent and Trademark Office connected therewith. (List name and registration number.)

| | | | |
|---------------------|-----------------|--------------------|-----------------|
| Carl W. Battle | Reg. No. 30,731 | Anita W. Magatti | Reg. No. 29,825 |
| Edwin P. Ching | Reg. No. 34,090 | John J. Maitner | Reg. No. 25,636 |
| Eric S. Dicker | Reg. No. 31,699 | Joseph T. Majka | Reg. No. 30,570 |
| Norman C. Dulak | Reg. No. 31,608 | Arthur Mann | Reg. No. 35,598 |
| Cynthia L. Foulke | Reg. No. 32,364 | Edward H. Mazer | Reg. No. 27,573 |
| Robert A. Franks | Reg. No. 28,605 | Jaye P. McLaughlin | Reg. No. 41,211 |
| James M. Gould | Reg. No. 33,702 | Richard B. Murphy | Reg. No. 35,298 |
| Richard J. Grochala | Reg. No. 31,518 | James R. Nelson | Reg. No. 27,929 |
| Thomas D. Hoffman | Reg. No. 28,221 | Immac J. Thampoe | Reg. No. 36,322 |
| Henry C. Jeanette | Reg. No. 30,856 | Paul A. Thompson | Reg. No. 35,385 |
| Susan Lee | Reg. No. 30,653 | Donald W. Wyatt | Reg. No. 40,879 |

| | |
|--|---|
| Send Correspondence to: Edwin P. Ching DNAX Research Institute 901 California Avenue Palo Alto, CA 94304-1104 | Direct Telephone Calls to: Name: Edwin P. Ching Telephone No.: (650) 496-1204 Facsimile No.: (650) 496-1200 |
|--|---|

| | | | |
|--|----------------------------|---------------------------------|-------------------------------------|
| FULL NAME OF 1ST OR SOLE INVENTOR | FAMILY NAME | FIRST GIVEN NAME | SECOND GIVEN NAME |
| | Bates | Elizabeth | Esther Mary |
| RESIDENCE & CITIZENSHIP | CITY | STATE OR FOREIGN COUNTRY | COUNTRY OF CITIZENSHIP |
| | Lyon | France | United Kingdom |
| POST OFFICE ADDRESS | POST OFFICE ADDRESS | CITY | STATE & ZIP CODE/COUNTRY |
| | 13, rue Terme | Lyon | France 69001 |

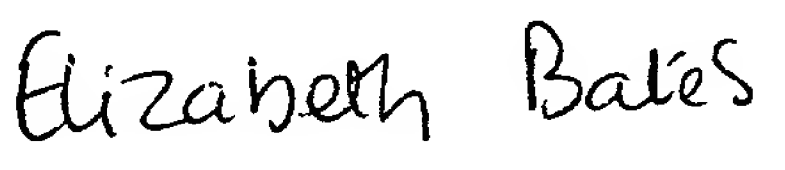
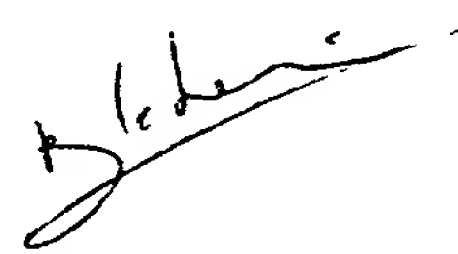
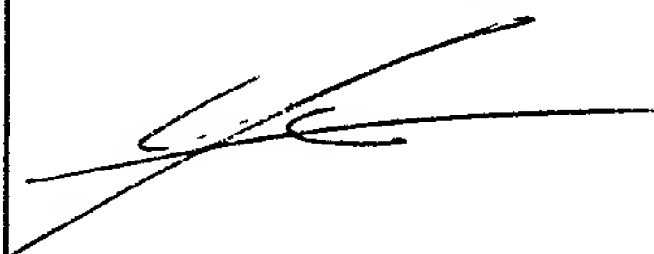
| | | | |
|--|----------------------------|---------------------------------|-------------------------------------|
| FULL NAME OF 2ND JOINT INVENTOR | FAMILY NAME | FIRST GIVEN NAME | SECOND GIVEN NAME |
| | de Saint-Vis | Blandine | Marie |
| RESIDENCE & CITIZENSHIP | CITY | STATE OR FOREIGN COUNTRY | COUNTRY OF CITIZENSHIP |
| | Lyon | France | France |
| POST OFFICE ADDRESS | POST OFFICE ADDRESS | CITY | STATE & ZIP CODE/COUNTRY |
| | 76, rue d'Anvers | Lyon | France 69007 |

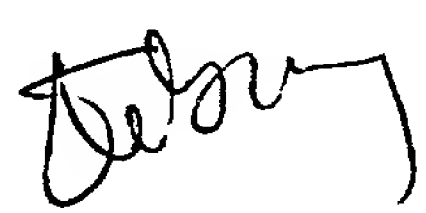

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|--|----------------------------|---------------------------------|-------------------------------------|
| FULL NAME OF 3RD JOINT INVENTOR | FAMILY NAME | FIRST GIVEN NAME | SECOND GIVEN NAME |
| | Caux | Christophe | |
| RESIDENCE & CITIZENSHIP | CITY | STATE OR FOREIGN COUNTRY | COUNTRY OF CITIZENSHIP |
| | France | Lyon | France |
| POST OFFICE ADDRESS | POST OFFICE ADDRESS | CITY | STATE & ZIP CODE/COUNTRY |
| | 1, rue de Savoie | Lyon | France 69002 |

| | | | |
|---------------------------------|--|------------------------------------|--|
| FULL NAME OF 4TH JOINT INVENTOR | FAMILY NAME Lebecque | FIRST GIVEN NAME Serge | SECOND GIVEN NAME J. E. |
| RESIDENCE & CITIZENSHIP | CITY Civrieux d' Azergue | STATE OR FOREIGN COUNTRY France | COUNTRY OF CITIZENSHIP Belgium |
| POST OFFICE ADDRESS | POST OFFICE ADDRESS 514, Chemin du Marand | CITY Civrieux d' Azergue | STATE & ZIP CODE/COUNTRY France 69380 |

| | | | |
|---------------------------------|------------------------------------|-----------------------------------|---|
| FULL NAME OF 5TH JOINT INVENTOR | FAMILY NAME Banchereau | FIRST GIVEN NAME Jacques | SECOND GIVEN NAME . |
| RESIDENCE & CITIZENSHIP | CITY Dallas | STATE OR FOREIGN COUNTRY Texas | COUNTRY OF CITIZENSHIP France |
| POST OFFICE ADDRESS | POST OFFICE ADDRESS 2752 Gaston | CITY Dallas | STATE & ZIP CODE/COUNTRY Texas 75226 |

I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

| | | |
|--|--|--|
| Signature of First Inventor  | Signature of Second Inventor  | Signature of Third Inventor  |
| Elizabeth Esther Mary Bates | Blandine Marie de Saint-Vis | Christophe Caux |
| Date 13/02/98 | Date 16/2/98 | Date 13/02/98 |

| | |
|---|---|
| Signature of Fourth Inventor  | Signature of Fifth Inventor  |
| Serge J.E. Lebecque | Jacques Banchereau |
| Date 16/02/1998 | Date |

| | | | |
|---------------------------------|--|------------------------------------|--|
| FULL NAME OF 4TH JOINT INVENTOR | FAMILY NAME Lebecque | FIRST GIVEN NAME Serge | SECOND GIVEN NAME J. E. |
| RESIDENCE & CITIZENSHIP | CITY Civrieux d' Azergue | STATE OR FOREIGN COUNTRY France | COUNTRY OF CITIZENSHIP Belgium |
| POST OFFICE ADDRESS | POST OFFICE ADDRESS 514. Chemin du Marand | CITY Civrieux d' Azergue | STATE & ZIP CODE/COUNTRY France 69380 |

| | | | |
|---------------------------------|------------------------------------|-----------------------------------|---|
| FULL NAME OF 5TH JOINT INVENTOR | FAMILY NAME Banchereau | FIRST GIVEN NAME Jacques | SECOND GIVEN NAME . |
| RESIDENCE & CITIZENSHIP | CITY Dallas | STATE OR FOREIGN COUNTRY Texas | COUNTRY OF CITIZENSHIP France |
| POST OFFICE ADDRESS | POST OFFICE ADDRESS 2752 Gaston | CITY Dallas | STATE & ZIP CODE/COUNTRY Texas 75226 |

I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

| | | |
|-----------------------------|------------------------------|-----------------------------|
| Signature of First Inventor | Signature of Second Inventor | Signature of Third Inventor |
| Elizabeth Esther Mary Bates | Blandine Marie de Saint-Vis | Christophe Caux |
| Date | Date | Date |

| | |
|------------------------------|--|
| Signature of Fourth Inventor | Signature of Fifth Inventor <i>Jacques Banchereau</i> |
| Serge J.E. Lebecque | Jacques Banchereau |
| Date | Date <i>28 January 1998.</i> |

SEQUENCE SUBMISSION

5 SEQ ID NO: 1 is human A05F12 diubiquitin nucleotide sequence.
SEQ ID NO: 2 is human A05F12 diubiquitin polypeptide sequence.
SEQ ID NO: 3 is mouse A05F12 diubiquitin nucleotide sequence.
SEQ ID NO: 4 is mouse A05F12 diubiquitin polypeptide sequence.
SEQ ID NO: 5 is human A07C03 Ig family gene nucleotide sequence.
10 SEQ ID NO: 6 is human A07C03 Ig family gene polypeptide sequence.
SEQ ID NO: 7 is revised human A07C03 Ig family gene nucleotide sequence.
SEQ ID NO: 8 is revised human A07C03 Ig family gene polypeptide sequence.
SEQ ID NO: 9 is mouse A07C03 Ig family gene nucleotide sequence.
SEQ ID NO: 10 is mouse A07C03 Ig family gene polypeptide sequence.
15 SEQ ID NO: 11 is human E02B02 LAMP-like gene nucleotide sequence.
SEQ ID NO: 12 is human E02B02 LAMP-like gene polypeptide sequence.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Bates, Elizabeth E.M.
de Saint-Vis, Blandine M.
25 Caux, Christophe
Lebecque, Serge J.E.
Banchereau, Jacques

(ii) TITLE OF INVENTION: ISOLATED MAMMALIAN DENDRITIC CELL GENES;
30 RELATED REAGENTS

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DNAX Research Institute
(B) STREET: 901 California Avenue
(C) CITY: Palo Alto
(D) STATE: California
(E) COUNTRY: USA
40 (F) ZIP: 94304-1104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
45 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
50 (B) FILING DATE: 25-NOV-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/032,767
55 (B) FILING DATE: 11-DEC-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/031,806

(B) FILING DATE: 27-NOV-1996

5

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ching, Edwin P.

(B) REGISTRATION NUMBER: 34,090

(C) REFERENCE/DOCKET NUMBER: DX0669K

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650)852-9196

(B) TELEFAX: (650)496-1204

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 777 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: cDNA

25

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 19..513

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCCCCTTGT CTGCAGAG ATG GCT CCC AAT GCT TCC TGC CTC TGT GTG CAT 51
Met Ala Pro Asn Ala Ser Cys Leu Cys Val His
1 5 10

GTC CGT TCC GAG GAA TGG GAT TTA ATG ACC TTT GAT GCC AAC CCA TAT 99
Val Arg Ser Glu Glu Trp Asp Leu Met Thr Phe Asp Ala Asn Pro Tyr
15 20 25

GAC AGC GTG AAA AAA ATC AAA GAA CAT GTC CGG TCT AAG ACC AAG GTT 147
Asp Ser Val Lys Lys Ile Lys Glu His Val Arg Ser Lys Thr Lys Val
30 35 40

CCT GTG CAG GAC CAG GTT CTT TTG CTG GGC TCC AAG ATC TTA AAG CCA 195
Pro Val Gln Asp Gln Val Leu Leu Leu Gly Ser Lys Ile Leu Lys Pro
45 50 55

CGG AGA AGC CTC TCA TCT TAT GGC ATT GAC AAA GAG AAG ACC ATC CAC 243
Arg Arg Ser Leu Ser Ser Tyr Gly Ile Asp Lys Glu Lys Thr Ile His
60 65 70 75

CTT ACC CTG AAA GTG GTG AAG CCC AGT GAT GAG GAG CTG CCC TTG TTT 291
Leu Thr Leu Lys Val Val Lys Pro Ser Asp Glu Glu Leu Pro Leu Phe
80 85 90

55

T0267444660

CTT GTG GAG TCA GGT GAT GAG GCA AAG AGG CAC CTC CTC CAG GTG CGA 339
Leu Val Glu Ser Gly Asp Glu Ala Lys Arg His Leu Leu Gln Val Arg
95 100 105

AGG TCC AGC TCA GTG GCA CAA GTG AAA GCA ATG ATC GAG ACT AAG ACG 387
Arg Ser Ser Ser Val Ala Gln Val Lys Ala Met Ile Glu Thr Lys Thr
110 115 120

GGT ATA ATC CCT GAG ACC CAG ATT GTG ACT TGC AAT GGA AAG AGA CTG 435
Gly Ile Ile Pro Glu Thr Gln Ile Val Thr Cys Asn Gly Lys Arg Leu
125 130 135

GAA GAT GGG AAG ATG ATG GCA GAT TAC GGC ATC AGA AAG GGC AAC TTA 483
Glu Asp Gly Lys Met Met Ala Asp Tyr Gly Ile Arg Lys Gly Asn Leu
140 145 150 155

CTC TTC CTG GCA TCT TAT TGT ATT GGA GGG TGACCACCCT GGGGATGGGG 533
Leu Phe Leu Ala Ser Tyr Cys Ile Gly Gly
160 165

TGTTGGCAGG GGTCAAAAAG CTTATTTCTT TTAATCTCTT ACTCAACGAA CACATCTTCT 593

GATGATTTCC CAAAATTAAT GAGAATGAGA TGAGTAGAGT AAGATTTGGG TGGGATGGGT 653

AGGATGAAGT ATATTGCCCA ACTCTATGTT TCTTTGATTC TAACACAATT AATTAAGTGA 713

CATGATTTTT ACTAATGTAT TACTGAGACT AGTAAATAAA TTTTAAAGGC AAAATAGAGC 773

ATTC 777

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Pro Asn Ala Ser Cys Leu Cys Val His Val Arg Ser Glu Glu
1 5 10 15

Trp Asp Leu Met Thr Phe Asp Ala Asn Pro Tyr Asp Ser Val Lys Lys
20 25 30

Ile Lys Glu His Val Arg Ser Lys Thr Lys Val Pro Val Gln Asp Gln
35 40 45

Val Leu Leu Leu Gly Ser Lys Ile Leu Lys Pro Arg Arg Ser Leu Ser
50 55 60

Ser Tyr Gly Ile Asp Lys Glu Lys Thr Ile His Leu Thr Leu Lys Val
65 70 75 80

Val Lys Pro Ser Asp Glu Glu Leu Pro Leu Phe Leu Val Glu Ser Gly
85 90 95

Asp Glu Ala Lys Arg His Leu Leu Gln Val Arg Arg Ser Ser Ser Val
100 105 110

Ala Gln Val Lys Ala Met Ile Glu Thr Lys Thr Gly Ile Ile Pro Glu
115 120 125

Thr Gln Ile Val Thr Cys Asn Gly Lys Arg Leu Glu Asp Gly Lys Met
130 135 140

Met Ala Asp Tyr Gly Ile Arg Lys Gly Asn Leu Leu Phe Leu Ala Ser
145 150 155 160

Tyr Cys Ile Gly Gly
165

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 8..493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TACAGAC ATG GCT TCT GTC CGC ACC TGT GTT GTC CGT TCA GAC CAA TGG 49
Met Ala Ser Val Arg Thr Cys Val Val Arg Ser Asp Gln Trp
1 5 10

CGG TTA ATG ACC TTT GAG ACC ACT GAG AAT GAC AAA GTG AAG AAG ATA 97
Arg Leu Met Thr Phe Glu Thr Thr Glu Asn Asp Lys Val Lys Lys Ile
15 20 25 30

AAT GAA CAT ATT AGG TCC CAA ACC AAG GTC TCT GTA CAG GAC CAG ATC 145
Asn Glu His Ile Arg Ser Gln Thr Lys Val Ser Val Gln Asp Gln Ile
35 40 45

CTT CTG CTA GAC TCC AAA ATC CTC AAG CCC CAT CGA AAA TTG TCA TCC 193
Leu Leu Leu Asp Ser Lys Ile Leu Lys Pro His Arg Lys Leu Ser Ser
50 55 60

TAT GGG ATT GAC AAG GAA ACC ACT ATC CAC CTT ACC CTG AAG GTG GTG 241
 Tyr Gly Ile Asp Lys Glu Thr Thr Ile His Leu Thr Leu Lys Val Val
 65 70 75
 5 AAG CCC AGT GAT GAA GAG CTG CCC TTG TTT CTG GTG GAG TCC AAA AAC 289
 Lys Pro Ser Asp Glu Glu Leu Pro Leu Phe Leu Val Glu Ser Lys Asn
 80 85 90
 10 GAG GGG CAA AGG CAC CTC CTC CGA GTT CGA AGA TCC AGC TCA GTG GCC 337
 Glu Gly Gln Arg His Leu Leu Arg Val Arg Arg Ser Ser Ser Val Ala
 95 100 105 110
 15 CAG GTG AAA GAG ATG ATC GAG AGT GTG ACC TCT GTG ATC CCT AAG AAG 385
 Gln Val Lys Glu Met Ile Glu Ser Val Thr Ser Val Ile Pro Lys Lys
 115 120 125
 CAG GTT GTG AAT TGC AAC GGA AAG AAG CTG GAA GAT GGA AAG ATC ATG 433
 Gln Val Val Asn Cys Asn Gly Lys Lys Leu Glu Asp Gly Lys Ile Met
 130 135 140
 20 GCT GAC TAC AAC ATC AAG AGT GGC AGT TTG CTC TTT CTG ACA ACA CAC 481
 Ala Asp Tyr Asn Ile Lys Ser Gly Ser Leu Leu Phe Leu Thr Thr His
 145 150 155
 25 TGC ACT GGG GGA TGA 496
 Cys Thr Gly Gly
 160

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Ser Val Arg Thr Cys Val Val Arg Ser Asp Gln Trp Arg Leu
 1 5 10 15
 Met Thr Phe Glu Thr Thr Glu Asn Asp Lys Val Lys Lys Ile Asn Glu
 20 25 30
 His Ile Arg Ser Gln Thr Lys Val Ser Val Gln Asp Gln Ile Leu Leu
 35 40 45
 50 Leu Asp Ser Lys Ile Leu Lys Pro His Arg Lys Leu Ser Ser Tyr Gly
 50 55 60
 Ile Asp Lys Glu Thr Thr Ile His Leu Thr Leu Lys Val Val Lys Pro
 65 70 75 80

5 Ser Asp Glu Glu Leu Pro Leu Phe Leu Val Glu Ser Lys Asn Glu Gly
85 90 95
Gln Arg His Leu Leu Arg Val Arg Arg Ser Ser Ser Val Ala Gln Val
100 105 110
Lys Glu Met Ile Glu Ser Val Thr Ser Val Ile Pro Lys Lys Gln Val
115 120 125
10 Val Asn Cys Asn Gly Lys Lys Leu Glu Asp Gly Lys Ile Met Ala Asp
130 135 140
Tyr Asn Ile Lys Ser Gly Ser Leu Leu Phe Leu Thr Thr His Cys Thr
145 150 155 160
15 Gly Gly

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1040 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 45..767

- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 111..767

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

40 TTCCTTTCAA ATACACACCC CAACCCGCCC CGGCATACAC AGAA ATG GGG ACT GCG 56
Met Gly Thr Ala
-22 -20
45 AGC AGA AGC AAC ATC GCT CGC CAT CTG CAA ACC AAT CTC ATT CTA TTT 104
Ser Arg Ser Asn Ile Ala Arg His Leu Gln Thr Asn Leu Ile Leu Phe
-15 -10 -5
50 TGT GTC GGT GCT GTG GGC GCC TGT ACT CTC TCT GTC ACA CAA CCG TGG 152
Cys Val Gly Ala Val Gly Ala Cys Thr Leu Ser Val Thr Gln Pro Trp
1 5 10
TAC CTA GAA GTG GAC TAC ACT CAT GAG GCC GTC ACC ATA AAG TGT ACC 200
Tyr Leu Glu Val Asp Tyr Thr His Glu Ala Val Thr Ile Lys Cys Thr
15 20 25 30
55

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|----|---|-----|
| 5 | TTC TCC GCA ACC GGA TGC CCT TCT GAG CAA CCA ACA TGC CTG TGG TTT Phe Ser Ala Thr Gly Cys Pro Ser Glu Gln Pro Thr Cys Leu Trp Phe 35 40 45 | 248 |
| 10 | CGC TAC GGT GCT CAC CAG CCT GAG AAC CTG TGC TTG GAC GGG TGC AAA Arg Tyr Gly Ala His Gln Pro Glu Asn Leu Cys Leu Asp Gly Cys Lys 50 55 60 | 296 |
| 15 | AGT GAG GCA GAC AAG TTC ACA GTG AGG GAG GCC CTC AAA GAA AAC CAA Ser Glu Ala Asp Lys Phe Thr Val Arg Glu Ala Leu Lys Glu Asn Gln 65 70 75 | 344 |
| 20 | GTT TCC CTC ACT GTA AAC AGA GTG ACT TCA AAT GAC AGT GCA ATT TAC Val Ser Leu Thr Val Asn Arg Val Thr Ser Asn Asp Ser Ala Ile Tyr 80 85 90 | 392 |
| 25 | ATC TGT GGA ATA GCA TTC CCC AGT GTG CCG GAA GCG AGA GCT AAA CAG Ile Cys Gly Ile Ala Phe Pro Ser Val Pro Glu Ala Arg Ala Lys Gln 95 100 105 110 | 440 |
| 30 | ACA GGA GGA GGG ACC ACA CTG GTG GTA AGA GAA ATT AAG CTG CTC AGC Thr Gly Gly Gly Thr Thr Leu Val Val Arg Glu Ile Lys Leu Leu Ser 115 120 125 | 488 |
| 35 | AAG GAA CTG CGG AGC TTC CTG ACA GCT CTT GTA TCA CTG CTC TCT GTC Lys Glu Leu Arg Ser Phe Leu Thr Ala Leu Val Ser Leu Leu Ser Val 130 135 140 | 536 |
| 40 | TAT GTG ACC GGT GTG TGC GTG GCC TTC ATA CTC CTC TCC AAA TCA AAA Tyr Val Thr Gly Val Cys Val Ala Phe Ile Leu Leu Ser Lys Ser Lys 145 150 155 | 584 |
| 45 | TCC AAC CCT CTA AGA AAG AAA GAA ATA AAA GAA GAC TCA CAA AAG AAG Ser Asn Pro Leu Arg Lys Lys Glu Ile Lys Glu Asp Ser Gln Lys Lys 160 165 170 | 632 |
| 50 | AAG AGT GCT CGG CGT ATT TTT CAG GAA ATT GCT CAA GAA CTA TAC CAT Lys Ser Ala Arg Arg Ile Phe Gln Glu Ile Ala Gln Glu Leu Tyr His 175 180 185 190 | 680 |
| 55 | AAG AGA CAT GTG GAA ACA AAT CAG CAA TCT GAG AAA GAT AAC AAC ACT Lys Arg His Val Glu Thr Asn Gln Gln Ser Glu Lys Asp Asn Asn Thr 195 200 205 | 728 |
| | TAT GAA AAC AGA AGA GTA CTT TCC AAC TAT GAA AGG CCA TAGAAACGTT Tyr Glu Asn Arg Arg Val Leu Ser Asn Tyr Glu Arg Pro 210 215 | 777 |
| | TTAATTTTCA ATGAAGTCAC TGAAAATCCA ACTCCAGGAG CTATGGCAGT GTTAATGAAC | 837 |
| | ATATATCATC AGGTCTTAAA AAAAAAATAA AGGTAACTG AAAAGACAAC TGGCTACAAA | 897 |
| | GAAGGATGTC AGAATGTAAG GAAACTATAA CTAATAGTCA TTACCAAAAT ACTAAAACCC | 957 |

AACAAAATGC AACTGAAAAA TACCTTCCAA ATTTGCCAAG AAAAAAATT CTATTAACT 1017
AAAAAAAAAA AAAAAAAAAA AAA 1040

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 241 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Thr Ala Ser Arg Ser Asn Ile Ala Arg His Leu Gln Thr Asn
-22 -20 -15 -10

Leu Ile Leu Phe Cys Val Gly Ala Val Gly Ala Cys Thr Leu Ser Val
-5 1 5 10

Thr Gln Pro Trp Tyr Leu Glu Val Asp Tyr Thr His Glu Ala Val Thr
15 20 25

Ile Lys Cys Thr Phe Ser Ala Thr Gly Cys Pro Ser Glu Gln Pro Thr
30 35 40

Cys Leu Trp Phe Arg Tyr Gly Ala His Gln Pro Glu Asn Leu Cys Leu
45 50 55

Asp Gly Cys Lys Ser Glu Ala Asp Lys Phe Thr Val Arg Glu Ala Leu
60 65 70

Lys Glu Asn Gln Val Ser Leu Thr Val Asn Arg Val Thr Ser Asn Asp
75 80 85 90

Ser Ala Ile Tyr Ile Cys Gly Ile Ala Phe Pro Ser Val Pro Glu Ala
95 100 105

Arg Ala Lys Gln Thr Gly Gly Gly Thr Thr Leu Val Val Arg Glu Ile
110 115 120

Lys Leu Leu Ser Lys Glu Leu Arg Ser Phe Leu Thr Ala Leu Val Ser
125 130 135

Leu Leu Ser Val Tyr Val Thr Gly Val Cys Val Ala Phe Ile Leu Leu
140 145 150

Ser Lys Ser Lys Ser Asn Pro Leu Arg Lys Lys Glu Ile Lys Glu Asp
155 160 165 170

Ser Gln Lys Lys Lys Ser Ala Arg Arg Ile Phe Gln Glu Ile Ala Gln
175 180 185

55

Glu Leu Tyr His Lys Arg His Val Glu Thr Asn Gln Gln Ser Glu Lys
190 195 200

Asp Asn Asn Thr Tyr Glu Asn Arg Arg Val Leu Ser Asn Tyr Glu Arg
205 210 215

Pro

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1042 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 45..767

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
(B) LOCATION: 111..767

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1013
(D) OTHER INFORMATION: /note= "nucleotides 1013 and 1014
are designated C, but may be C or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTCCTTTCAA ATACACACCC CAACCCGCCC CGGCATACAC AGAA ATG GGG ACT GCG 56
Met Gly Thr Ala
-22 -20

AGC AGA AGC AAC ATC GCT CGC CAT CTG CAA ACC AAT CTC ATT CTA TTT 104
Ser Arg Ser Asn Ile Ala Arg His Leu Gln Thr Asn Leu Ile Leu Phe
-15 -10 -5

TGT GTC GGT GCT GTG GGC GCC TGT ACT CTC TCT GTC ACA CAA CCG TGG 152
Cys Val Gly Ala Val Gly Ala Cys Thr Leu Ser Val Thr Gln Pro Trp
1 5 10

TAC CTA GAA GTG GAC TAC ACT CAT GAG GCC GTC ACC ATA AAG TGT ACC 200
Tyr Leu Glu Val Asp Tyr Thr His Glu Ala Val Thr Ile Lys Cys Thr
15 20 25 30

CTAAAAAAAA AAAAAAAAAA AAAAA

1042

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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

15

Met Gly Thr Ala Ser Arg Ser Asn Ile Ala Arg His Leu Gln Thr Asn
-22 -20 -15 -10

Leu Ile Leu Phe Cys Val Gly Ala Val Gly Ala Cys Thr Leu Ser Val
-5 1 5 10

20

Thr Gln Pro Trp Tyr Leu Glu Val Asp Tyr Thr His Glu Ala Val Thr
15 20 25

Ile Lys Cys Thr Phe Ser Ala Thr Gly Cys Pro Ser Glu Gln Pro Thr
30 35 40

25

Cys Leu Trp Phe Arg Tyr Gly Ala His Gln Pro Glu Asn Leu Cys Leu
45 50 55

Asp Gly Cys Lys Ser Glu Ala Asp Lys Phe Thr Val Arg Glu Ala Leu
60 65 70

Lys Glu Asn Gln Val Ser Leu Thr Val Asn Arg Val Thr Ser Asn Asp
75 80 85 90

35

Ser Ala Ile Tyr Ile Cys Gly Ile Ala Phe Pro Ser Val Pro Glu Ala
95 100 105

Arg Ala Lys Gln Thr Gly Gly Gly Thr Thr Leu Val Val Arg Glu Ile
110 115 120

40

Lys Leu Leu Ser Lys Glu Leu Arg Ser Phe Leu Thr Ala Leu Val Ser
125 130 135

Leu Leu Ser Val Tyr Val Thr Gly Val Cys Val Ala Phe Ile Leu Leu
140 145 150

45

Ser Lys Ser Lys Ser Asn Pro Leu Arg Lys Lys Glu Ile Lys Glu Asp
155 160 165 170

50

Ser Gln Lys Lys Lys Ser Ala Arg Arg Ile Phe Gln Glu Ile Ala Gln
175 180 185

Glu Leu Tyr His Lys Arg His Val Glu Thr Asn Gln Gln Ser Glu Lys
190 195 200

Asp Asn Asn Thr Tyr Glu Asn Arg Arg Val Leu Ser Asn Tyr Glu Arg
205 210 215

Pro

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 37..750

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
(B) LOCATION: 103..750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCACGCGTCC GGGAAAAGGC GGCACATGCA CCAGCG ATG GGC CCT GTG AGC ACG 54
Met Gly Pro Val Ser Thr
-22 -20

AGC AGG AGG GGC CTC CGG CTA GGA ATC AGC CTG ATC CTT CTT CAA GTT 102
Ser Arg Arg Gly Leu Arg Leu Gly Ile Ser Leu Ile Leu Leu Gln Val
-15 -10 -5

GGT GTG GTG GGC GCC TGT ACT GTA TCT GTG CTA CAG CCA GGT TAC CTA 150
Gly Val Val Gly Ala Cys Thr Val Ser Val Leu Gln Pro Gly Tyr Leu
1 5 10 15

GAG GTG GAC TAC ACG TCT CAG ACT GTC ACC ATG GAG TGT ACC TTT TCT 198
Glu Val Asp Tyr Thr Ser Gln Thr Val Thr Met Glu Cys Thr Phe Ser
20 25 30

ACA ACT GGA TGC CCT GCA GTG CAA CCA AAA AGC TTG TGG TTT CGC TGT 246
Thr Thr Gly Cys Pro Ala Val Gln Pro Lys Ser Leu Trp Phe Arg Cys
35 40 45

GGC ACT CAC CAG CCT GAA GCT CTG TGC TTG GAC GGA TGC AGA AAT GAG 294
Gly Thr His Gln Pro Glu Ala Leu Cys Leu Asp Gly Cys Arg Asn Glu
50 55 60

5 GCA GAC AAG TTC ACA GTG AAA GAA ACC CTG GAC CAG AAC CGA GTC TCC 342
Ala Asp Lys Phe Thr Val Lys Glu Thr Leu Asp Gln Asn Arg Val Ser
65 70 75 80

10 CTC ACT GTT AAC AGG CTG TCT CCA AAT GAC AGT GCA ATC TAC ATC TGT 390
Leu Thr Val Asn Arg Leu Ser Pro Asn Asp Ser Ala Ile Tyr Ile Cys
85 90 95

15 GGA ATA GCA TTT CCC AAT GAA CCG GTA CCA ACA GCC AAA CAG ACT GGA 438
Gly Ile Ala Phe Pro Asn Glu Pro Val Pro Thr Ala Lys Gln Thr Gly
100 105 110

20 GAC GGG ACT ACA CTG GTG GTA AGA GAA AGA CTT TTC AGC AGG GAG GTG 486
Asp Gly Thr Thr Leu Val Val Arg Glu Arg Leu Phe Ser Arg Glu Val
115 120 125

25 CAC AGT CTC CTG ATA GTG CTC TTA GCA CTG CTC GCA GTC TAC GTC ACC 534
His Ser Leu Leu Ile Val Leu Leu Ala Leu Leu Ala Val Tyr Val Thr
130 135 140

30 GGT GTG TGT GTG ATC TTC ATA GTC CTC TTC AGA TCA AAA TCT AAC ACT 582
Gly Val Cys Val Ile Phe Ile Val Leu Phe Arg Ser Lys Ser Asn Thr
145 150 155 160

35 CCA AGA AGC AGA GAA ACC AAG GAA GAC TCG AAA AAG AAG AGT GCT CGA 630
Pro Arg Ser Arg Glu Thr Lys Glu Asp Ser Lys Lys Lys Ser Ala Arg
165 170 175

40 CGT ATC TTC CAG GAA ATT GCT CAA GAA TTA TAC CAT AAG AGA TAT GTG 678
Arg Ile Phe Gln Glu Ile Ala Gln Glu Leu Tyr His Lys Arg Tyr Val
180 185 190

45 GAA ACA AGT CAT CAG CCT GAG CAA GAC GGC AAT TAT GAA AAC AGA AAA 726
Glu Thr Ser His Gln Pro Glu Gln Asp Gly Asn Tyr Glu Asn Arg Lys
195 200 205

50 GCA CTC CCC AGC CCT GGA AGA CCA TAGATGTGCT GACTTTTTTAC TTAAACCATT 780
Ala Leu Pro Ser Pro Gly Arg Pro
210 215

55 GACAGTGCAA CTCCAGAATC TATGGCAGTG TGAATGGACA TACAGCAATC CAAACAACAG 840

CAAAGAGAGC TGAGGTGTAG CTTGAGTGGC AAAGTGCTTG CCCAGTAGGC ATGAAGTCTT 900

AGCTTTGATC CTCAGCACCA CATAACTCAG CAAAGTGACA CAAGCCTGTA TTCCCAACAT 960

TGTGTAGTAG TATAAAAAGT CAGAAGTTCA AGGTCATCCC TGACTATAGG ATGAACCTGA 1020

AGTCAGAGAC ATGTTATCTT GTCTCAAAAA CACTGCCACC ACCAAGAGAA AAGGGCAGGA 1080

CAAGTGGGAA AACAGCCAGT CACGCCAGAA GGCAGAGCGG AAGTAACTGT CACGAACCAT 1140

AATGATGGAA TGTGAAAACC TCAAGAAAAC TCAACTGGAG GACCTTTTTT CTAATTTTCC 1200

AGGAACAGTC TAAGGAGCCT CATTTTAAAG AAAAAGTTCA CCTTCAGCTT TTA 1253

(2) INFORMATION FOR SEQ ID NO:10:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 238 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

15 Met Gly Pro Val Ser Thr Ser Arg Arg Gly Leu Arg Leu Gly Ile Ser
-22 -20 -15 -10

Leu Ile Leu Leu Gln Val Gly Val Val Gly Ala Cys Thr Val Ser Val
-5 1 5 10

20 Leu Gln Pro Gly Tyr Leu Glu Val Asp Tyr Thr Ser Gln Thr Val Thr
15 20 25

25 Met Glu Cys Thr Phe Ser Thr Thr Gly Cys Pro Ala Val Gln Pro Lys
30 35 40

30 Ser Leu Trp Phe Arg Cys Gly Thr His Gln Pro Glu Ala Leu Cys Leu
45 50 55

35 Asp Gly Cys Arg Asn Glu Ala Asp Lys Phe Thr Val Lys Glu Thr Leu
60 65 70

40 Asp Gln Asn Arg Val Ser Leu Thr Val Asn Arg Leu Ser Pro Asn Asp
75 80 85 90

45 Ser Ala Ile Tyr Ile Cys Gly Ile Ala Phe Pro Asn Glu Pro Val Pro
95 100 105

50 Thr Ala Lys Gln Thr Gly Asp Gly Thr Thr Leu Val Val Arg Glu Arg
110 115 120

55 Leu Phe Ser Arg Glu Val His Ser Leu Leu Ile Val Leu Leu Ala Leu
125 130 135

60 Leu Ala Val Tyr Val Thr Gly Val Cys Val Ile Phe Ile Val Leu Phe
140 145 150

65 Arg Ser Lys Ser Asn Thr Pro Arg Ser Arg Glu Thr Lys Glu Asp Ser
155 160 165 170

70 Lys Lys Lys Ser Ala Arg Arg Ile Phe Gln Glu Ile Ala Gln Glu Leu
175 180 185

75 Tyr His Lys Arg Tyr Val Glu Thr Ser His Gln Pro Glu Gln Asp Gly
190 195 200

80

Asn Tyr Glu Asn Arg Lys Ala Leu Pro Ser Pro Gly Arg Pro
205 210 215

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 43..1290

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 112..1290

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 481
- (D) OTHER INFORMATION: /note= "may be T"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 994
- (D) OTHER INFORMATION: /note= "may be A"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 49..51
- (D) OTHER INFORMATION: /note= "codon might be CGG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

| | |
|---|-----|
| CGCCCGGGCA GGTAGCGGCC GCTGAATTCT AGAACGCCCA CC ATG CCC CGG CAG | 54 |
| Met Pro Arg Gln | |
| -23 -20 | |
| CTC AGC GCG GCG GCC GCG CTC TTC GCG TCC CTG GCC GTA ATT TTG CAC | 102 |
| Leu Ser Ala Ala Ala Ala Leu Phe Ala Ser Leu Ala Val Ile Leu His | |
| -15 -10 -5 | |
| GAT GGC AGT CAA ATG AGA GCA AAA GCA TTT CCA GAA ACC AGA GAT TAT | 150 |
| Asp Gly Ser Gln Met Arg Ala Lys Ala Phe Pro Glu Thr Arg Asp Tyr | |
| 1 5 10 | |
| TCT CAA CCT ACT GCA GCA GCA ACA GTA CAG GAC ATA AAA AAA CCT GTC | 198 |
| Ser Gln Pro Thr Ala Ala Ala Thr Val Gln Asp Ile Lys Lys Pro Val | |
| 15 20 25 | |

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|----|---|-----|
| 5 | CAG CAA CCA GCT AAG CAA GCA CCT CAC CAA ACT TTA GCA GCA AGA TTC Gln Gln Pro Ala Lys Gln Ala Pro His Gln Thr Leu Ala Ala Arg Phe 30 35 40 45 | 246 |
| 10 | ATG GAT GGT CAT ATC ACC TTT CAA ACA GCG GCC ACA GTA AAA ATT CCA Met Asp Gly His Ile Thr Phe Gln Thr Ala Ala Thr Val Lys Ile Pro 50 55 60 | 294 |
| 15 | ACA ACT ACC CCA GCA ACT ACA AAA AAC ACT GCA ACC ACC AGC CCA ATT Thr Thr Thr Pro Ala Thr Thr Lys Asn Thr Ala Thr Thr Ser Pro Ile 65 70 75 | 342 |
| 20 | ACC TAC ACC CTG GTC ACA ACC CAG GCC ACA CCC AAC AAC TCA CAC ACA Thr Tyr Thr Leu Val Thr Thr Gln Ala Thr Pro Asn Asn Ser His Thr 80 85 90 | 390 |
| 25 | GCT CCT CCA GTT ACT GAA GTT ACA GTC GGC CCT AGC TTA GCC CCT TAT Ala Pro Pro Val Thr Glu Val Thr Val Gly Pro Ser Leu Ala Pro Tyr 95 100 105 | 438 |
| 30 | TCA CTG CCA CCC ACC ATC ACC CCA CCA GCT CAT ACA ACT GGA ACC AGT Ser Leu Pro Pro Thr Ile Thr Pro Pro Ala His Thr Thr Gly Thr Ser 110 115 120 125 | 486 |
| 35 | TCA TCA ACC GTC AGC CAC ACA ACT GGG AAC ACC ACT CAA CCC AGT AAC Ser Ser Thr Val Ser His Thr Thr Gly Asn Thr Thr Gln Pro Ser Asn 130 135 140 | 534 |
| 40 | CAG ACC ACC CTT CCA GCA ACT TTA TCG ATA GCA CTG CAC AAA AGC ACA Gln Thr Thr Leu Pro Ala Thr Leu Ser Ile Ala Leu His Lys Ser Thr 145 150 155 | 582 |
| 45 | ACC GGT CAG AAG CCT GTT CAA CCC ACC CAT GCC CCA GGA ACA ACG GCA Thr Gly Gln Lys Pro Val Gln Pro Thr His Ala Pro Gly Thr Thr Ala 160 165 170 | 630 |
| 50 | GCT GCC CAC AAT ACC ACC CGC ACA GCT GCA CCT GCC TCC ACG GTT CCT Ala Ala His Asn Thr Thr Arg Thr Ala Ala Pro Ala Ser Thr Val Pro 175 180 185 | 678 |
| | GGG CCC ACC CTT GCA CCT CAG CCA TCG TCA GTC AAG ACT GGA ATT TAT Gly Pro Thr Leu Ala Pro Gln Pro Ser Ser Val Lys Thr Gly Ile Tyr 190 195 200 205 | 726 |
| | CAG GTT CTA AAC GGA AGC AGA CTC TGT ATA AAA GCA GAG ATG GGG ATA Gln Val Leu Asn Gly Ser Arg Leu Cys Ile Lys Ala Glu Met Gly Ile 210 215 220 | 774 |
| | CAG CTG ATT GTT CAA GAC AAG GAG TCG GTT TTT TCA CCT CGG AGA TAC Gln Leu Ile Val Gln Asp Lys Glu Ser Val Phe Ser Pro Arg Arg Tyr 225 230 235 | 822 |

| | | |
|----|--|------|
| | TTC AAC ATC GAC CCC AAC GCA ACG CAA GCC TCT GGG AAC TGT GGC ACC | 870 |
| | Phe Asn Ile Asp Pro Asn Ala Thr Gln Ala Ser Gly Asn Cys Gly Thr | |
| | 240 245 250 | |
| 5 | CGA AAA TCC AAC CTT CTG TTG AAT TTT CAG GGC GGA TTT GTG AAT CTC | 918 |
| | Arg Lys Ser Asn Leu Leu Leu Asn Phe Gln Gly Gly Phe Val Asn Leu | |
| | 255 260 265 | |
| 10 | ACA TTT ACC AAG GAT GAA GAA TCA TAT TAT ATC AGT GAA GTG GGA GCC | 966 |
| | Thr Phe Thr Lys Asp Glu Glu Ser Tyr Tyr Ile Ser Glu Val Gly Ala | |
| | 270 275 280 285 | |
| 15 | TAT TTG ACC GTC TCA GAT CCA GAG ACA ATT TAC CAA GGA ATC AAA CAT | 1014 |
| | Tyr Leu Thr Val Ser Asp Pro Glu Thr Ile Tyr Gln Gly Ile Lys His | |
| | 290 295 300 | |
| | GCG GTG GTG ATG TTC CAG ACA GCA GTC GGG CAT TCC TTC AAG TGC GTG | 1062 |
| | Ala Val Val Met Phe Gln Thr Ala Val Gly His Ser Phe Lys Cys Val | |
| | 305 310 315 | |
| 20 | AGT GAA CAG AGC CTC CAG TTG TCA GCC CAC CTG CAG GTG AAA ACA ACC | 1110 |
| | Ser Glu Gln Ser Leu Gln Leu Ser Ala His Leu Gln Val Lys Thr Thr | |
| | 320 325 330 | |
| 25 | GAT GTC CAA CTT CAA GCC TTT GAT TTT GAA GAT GAC CAC TTT GGA AAT | 1158 |
| | Asp Val Gln Leu Gln Ala Phe Asp Phe Glu Asp Asp His Phe Gly Asn | |
| | 335 340 345 | |
| 30 | GTG GAT GAG TGC TCG TCT GAC TAC ACA ATT GTG CTT CCT GTG ATT GGG | 1206 |
| | Val Asp Glu Cys Ser Ser Asp Tyr Thr Ile Val Leu Pro Val Ile Gly | |
| | 350 355 360 365 | |
| 35 | GCC ATC GTG GTT GGT CTC TGC CTT ATG GGT ATG GGT GTC TAT AAA ATC | 1254 |
| | Ala Ile Val Val Gly Leu Cys Leu Met Gly Met Gly Val Tyr Lys Ile | |
| | 370 375 380 | |
| | CGC CTA AGG TGT CAA TCA TCT GGA TAC CAG AGA ATC TAATTGTTGC | 1300 |
| | Arg Leu Arg Cys Gln Ser Ser Gly Tyr Gln Arg Ile | |
| | 385 390 | |
| 40 | CCGGGGGGGAA TGAAAATAAT GGAATTTAGA GAACTCTTTC ATCCTTCCAG GATGGATGTT | 1360 |
| | GGAAATTCCC TCAGAGTGTG GGTCCTTCAA ACAATGTAAA CCACCATCTT CTATTCAAAT | 1420 |
| 45 | GAAGTGAGTC ATGTGTGATT TAAGTTCAGG CAGCACATCA ATTTCTAAAT ACTTTTTGTT | 1480 |
| | TATTTTATGA AAGATATAGT GAGCTGTTTA TTTTCTAGTT TCCTTTAGAA TATTTTAGCC | 1540 |
| | ACTCAAAGTC AACATTTGAG ATATGTTGAA TTAACATAAT ATATGTAAAG TAGAATAAGC | 1600 |
| 50 | CTTCAAATTA TAAACCAAGG GTCAATTGTA ACTAATACTA CTGTGTGTGC ATTGAAGATT | 1660 |
| | TTATTTTACC CTTGATCTTA ACAAAGCCTT TGCTTTGTTA TCAAATGGAC TTTCAGTGCT | 1720 |
| 55 | TTTACTATCT GTGTTTTATG GTTTCATGTA ACATACATAT TCCTGGTGTA GCACTTAACT | 1780 |

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CCTTTTCCAC TTAAATTTG TTTTGT TTTT TTGAGACGGA GTTTCAC TCT TGTCACCCAG 1840
GCTGGAGTAC AGTGGCACGA TCTCGGCTTA TGGCAACCTC CGCCTCCCGG GTTCAAGTGA 1900
TTCTCCTGCT TCAGCTTCCC GAGTAGCTGG GATTACAGGC ACACACTACC ACGCCTGGCT 1960
AATTTTTGTA TTTTATTAT AGACGGGGTT TCACCATGTT GGCCAGACTG GTCTTGAACT 2020
CTTGACCTCA GGTGATCCAC CCACCTCAGC CTCCCAAAGT GCTGGGATTA CAGGCATGAG 2080
CCATTGCGCC CGGCCTTAAA TGTTTTTTTTT AATCATCAAA AAGAACAACA TATCTCAGGT 2140
TGTCTAAGTG TTTTATGTA AAACCAACAA AAAGAACAAA TCAGCTTATA TTTTTTATCT 2200
TGATGACTCC TGCTCCAGAA TCGCTAGACT AAGAATTAGG TGGCTACAGA TGGTAGAACT 2260
AAACAATAAG CAAGAGACAA TAATAATGGC CCTTAATTAT TAACAAAGTG CCAGAGTCTA 2320
GGCTAAGCAC TTTATCTATA TCTCATTTCA TTCTCACAAC TTATAGGTGA ATGAGTAAAC 2380
TGAGACTTAA GGGAAGTGAA TCACTTAAAT GTCACCTGGC TAACTGATGG CAGAGCCAGA 2440
GCTTGAATTC ATGTTGGTCT GACATCAAGG TCTTTGGTCT TCTCCCTACA CCAAGTTACC 2500
TACAAGAACA ATGACACCAC ACTCTGCCTG AAGGCTCACA CCTCATACCA GCATACGCTC 2560
ACCTTACAGG GAAATGGGTT TATCCAGGAT CATGAGACAT TAGGGTAGAT GAAAGGAGAG 2620
CTTTGCAGAT AACAAAATAG CCTATCCTTA ATAAATCCTC CACTCTCTGG AAGGAGACTG 2680
AGGGGCTTTG TAAACATTA GTCAGTTGCT CATTTTTATG GGATTGCTTA GCTGGGCTGT 2740
AAAGATGAAG GCATCAAATA AACTCAAAGT ATTTTAAAT TTTTTTGATA ATAGAGAAAC 2800
TTCGCTAACC AACTGTTCTT TCTTGAGTGA TAGCCCCATC TTGTGGTAAC TTGCTGCTTC 2860
TGCACTTCAT ATCCATATTT CCTATTGTTC ACTTTATTCT GTAGAGCAGC CTGCCAAGAA 2920
TTTTATTTCT GCTGTTTTTTT TTGCTGCTAA AGAAAGGAAC TAAGTCAGGA TGTTAACAGA 2980
AAAGTCCACA TAACCCTAGA ATTCTTAGTC AAGGAATAAT TCAAGTCAGC CTAGAGACCA 3040
TGTTGACTTT CCTCATGTGT TTCCTTATGA CTCAGTAAGT TGGCAAGGTC CTGACTTTAG 3100
TCTTAATAAA ACATTGAATT GTAGTAAAGG TTTTGTAAAT AAAAAGTTAC TTTGGAAAAA 3160
AAAAAAAAAA AA 3172

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 416 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Pro Arg Gln Leu Ser Ala Ala Ala Ala Leu Phe Ala Ser Leu Ala
-23 -20 -15 -10

Val Ile Leu His Asp Gly Ser Gln Met Arg Ala Lys Ala Phe Pro Glu
-5 1 5

Thr Arg Asp Tyr Ser Gln Pro Thr Ala Ala Ala Thr Val Gln Asp Ile
10 15 20 25

Lys Lys Pro Val Gln Gln Pro Ala Lys Gln Ala Pro His Gln Thr Leu
30 35 40

Ala Ala Arg Phe Met Asp Gly His Ile Thr Phe Gln Thr Ala Ala Thr
45 50 55

Val Lys Ile Pro Thr Thr Thr Pro Ala Thr Thr Lys Asn Thr Ala Thr
60 65 70

Thr Ser Pro Ile Thr Tyr Thr Leu Val Thr Thr Gln Ala Thr Pro Asn
75 80 85

Asn Ser His Thr Ala Pro Pro Val Thr Glu Val Thr Val Gly Pro Ser
90 95 100 105

Leu Ala Pro Tyr Ser Leu Pro Pro Thr Ile Thr Pro Pro Ala His Thr
110 115 120

Thr Gly Thr Ser Ser Ser Thr Val Ser His Thr Thr Gly Asn Thr Thr
125 130 135

Gln Pro Ser Asn Gln Thr Thr Leu Pro Ala Thr Leu Ser Ile Ala Leu
140 145 150

His Lys Ser Thr Thr Gly Gln Lys Pro Val Gln Pro Thr His Ala Pro
155 160 165

Gly Thr Thr Ala Ala Ala His Asn Thr Thr Arg Thr Ala Ala Pro Ala
170 175 180 185

Ser Thr Val Pro Gly Pro Thr Leu Ala Pro Gln Pro Ser Ser Val Lys
190 195 200

Thr Gly Ile Tyr Gln Val Leu Asn Gly Ser Arg Leu Cys Ile Lys Ala
205 210 215

Glu Met Gly Ile Gln Leu Ile Val Gln Asp Lys Glu Ser Val Phe Ser
220 225 230

Pro Arg Arg Tyr Phe Asn Ile Asp Pro Asn Ala Thr Gln Ala Ser Gly
235 240 245

Asn Cys Gly Thr Arg Lys Ser Asn Leu Leu Leu Asn Phe Gln Gly Gly
250 255 260 265

Phe Val Asn Leu Thr Phe Thr Lys Asp Glu Glu Ser Tyr Tyr Ile Ser
270 275 280

Glu Val Gly Ala Tyr Leu Thr Val Ser Asp Pro Glu Thr Ile Tyr Gln
285 290 295

Gly Ile Lys His Ala Val Val Met Phe Gln Thr Ala Val Gly His Ser
300 305 310

Phe Lys Cys Val Ser Glu Gln Ser Leu Gln Leu Ser Ala His Leu Gln
315 320 325

Val Lys Thr Thr Asp Val Gln Leu Gln Ala Phe Asp Phe Glu Asp Asp
330 335 340 345

His Phe Gly Asn Val Asp Glu Cys Ser Ser Asp Tyr Thr Ile Val Leu
350 355 360

Pro Val Ile Gly Ala Ile Val Val Gly Leu Cys Leu Met Gly Met Gly
365 370 375

Val Tyr Lys Ile Arg Leu Arg Cys Gln Ser Ser Gly Tyr Gln Arg Ile
380 385 390